



SEQUENCE LISTING

<110> ANDREW, DAVID P.  
LEWIN, DAVID A.  
PENNICA, DIANE  
RASTELLI, LUCA  
TALLION, BRUCE

<120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC  
ACIDS ENCODING SAME

<130> 09800080-0104

<140> 10/614,599

<141> 2003-07-07

<150> 09/715,747

<151> 2000-11-17

<150> 09/715,418

<151> 2000-11-16

<150> 60/166,177

<151> 1999-11-18

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 212

<212> DNA

<213> Mus sp.

<400> 1

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tgtaatgact cgaaactgga gtttggaagg tt 212
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<210> 2

<211> 1670

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<213> Mus sp.

<220>

<221> misc\_feature

<222> (1541)

<223> "n" represents a, t, c, g, other or unknown

<400> 2

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ctcacagaag gaaggaccag tgtaccagga acgatgggac agtgctcggtc agccaatgct 180
gaggatgccc aagaattcag tgatgtagag agggccattg agacactcat caagaacttc 240
cataaatact ctgtggcgagg taaaaaggaa acactgaccc ctgctgagct tcgagacctg 300
gttaccacagc agctgccaca cctcatgccg agcaactgtg ggtagaaga gaaaattgcc 360
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aacctgggca actgtaatga ctcgaaactg gagtttggaa gcttctggga gttgattgga 420  
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 aatgcccacc acccccttcc ccagcctgca cctctcctca ttgctgcaat gttcacgttc 600  
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 agcaggggat ggaatctggc tgcataatth gtcccgaaaa ggggtgtctga gaacctacc 840  
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<210> 3  
 <211> 131  
 <212> PRT  
 <213> Mus sp.

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 20 25 30  
 Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala  
 35 40 45  
 Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys  
 50 55 60  
 Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln  
 65 70 75 80  
 Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala  
 85 90 95  
 Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp  
 100 105 110  
 Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val  
 115 120 125  
 Thr Arg Ser  
 130

<210> 4  
<211> 357  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (231)  
<223> "n" represents a, t, c, g, other or unknown

<220>  
<221> misc\_feature  
<222> (337)  
<223> "n" represents a, t, c, g, other or unknown

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catcaagaac tttcaccagt actccgtgga ggggtgggaag gagacgctga ccccttctga 180  
gctacgggac ctggtcaccc agcagctgcc ccatctcatg ccgagcaact ntggcctgga 240  
agagaaaatt gccaacctgg gcagctgcaa tgactctaaa ctggagttca ggagtttctg 300  
ggagctgatt ggagaagcgg ccaagagtgt gaagctngag aggactgtcc gggggca 357

<210> 5  
<211> 379  
<212> DNA  
<213> Homo sapiens

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caggttggca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180  
ggtgaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccaccct ccacggagta 240  
ctggtgaaag ttcttgatga ggggtctcaat ggccctctcc acatcactga attcctgagc 300  
atcctctgcg ttggctgacc gacactgtcc catggtgctc actgtgtctg gtcctttggc 360  
gagagttctg ttgtcctat 379

<210> 6  
<211> 118  
<212> PRT  
<213> Homo sapiens

<400> 6  
Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly  
1 5 10 15  
Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val  
20 25 30  
Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val  
35 40 45  
Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val  
50 55 60  
Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu

65                      70                      75                      80  
 Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg  
                             85                      90                      95  
 Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu  
                             100                      105                      110  
 Arg Pro Val Arg Gly His  
                             115

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 cttgatgagg gtctcaatgg 20

<210> 8  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Probe

<400> 8  
 ccacatcact gaattcctga gcatcc 26

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 cagacacagt gagcaccatg 20

<210> 10  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens, W27152, chemotactic cytokine II CCII from WO97/34013

<400> 10  
 Met Ala Ala Glu Pro Leu Thr Glu Leu Glu Glu Ser Ile Glu Thr Val  
   1                      5                      10                      15

Val Thr Thr Phe Phe Thr Phe Ala Arg Gln Glu Gly Arg Lys Asp Ser

20                      25                      30  
 Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His  
                     35                      40                      45  
 Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp  
                     50                      55                      60  
 Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile  
                     65                      70                      75                      80  
 Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg  
                     85                      90                      95

Lys Lys

<210> 11  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens, G491246, Macrophage Migration Inhibition Factor (MRP-14)

<400> 11  
 Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile Asn Thr Phe His  
                     1                      5                      10                      15  
 Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu  
                     20                      25                      30  
 Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu  
                     35                      40                      45  
 Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr  
                     50                      55                      60  
 Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala  
                     65                      70                      75                      80  
 Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly  
                     85                      90                      95  
 Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly Thr Pro  
                     100                      105                      110

<210> 12  
 <211> 37  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: 3-100/ICaBP type  
                     calcium binding protein

<400> 12  
 Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn  
                     1                      5                      10                      15

Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala  
20 25 30

Ala Lys Ser Val Lys  
35

<210> 13  
<211> 37  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: 3-100/ICaBP type  
calcium binding protein

<400> 13  
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr  
1 5 10 15

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp  
20 25 30

Leu Val Thr Gln Gln  
35

<210> 14  
<211> 19  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Bacterial type II  
secretion system protein F

<400> 14  
Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu  
1 5 10 15

Glu Lys Ile

<210> 15  
<211> 10  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Ubiquitin  
carboxyl-terminal hydrolases family

<400> 15  
Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser  
1 5 10

<210> 16  
<211> 49  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Bacterial  
themotaxis sensory transducers protein

<400> 16  
Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr  
1 5 10 15  
Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys  
20 25 30  
Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser  
35 40 45

Phe

<210> 17  
<211> 32  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:  
Phosphoenolpyruvate carboxykinase (ATP) protein

<400> 17  
Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser  
1 5 10 15  
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr  
20 25 30

<210> 18  
<211> 33  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Prokaryotic-type  
carbonic anhydrases proteins

<400> 18  
His Gln Tyr Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu  
1 5 10 15  
Leu Arg Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn  
20 25 30

Cys

<210> 19  
<211> 15  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Ergosterol  
biosynthesis ERG4/ERG24 family protein

<400> 19  
Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg  
1 5 10 15

<210> 20  
<211> 25  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:  
Lysosome-associated membrane glycoproteins du

<400> 20  
Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly  
1 5 10 15

Ser Cys Asn Asp Ser Lys Ile Glu Phe  
20 25

<210> 21  
<211> 39  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:  
Phosphofructokinase proteins

<400> 21  
Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys  
1 5 10 15

Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu  
20 25 30

Ala Ala Lys Ser Val Lys Leu  
35

<210> 22  
<211> 10  
<212> PRT  
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: PH domain  
proteins profile

<400> 22

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile  
1 5 10

<210> 23

<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Myotoxins  
protein

<400> 23

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys  
1 5 10 15

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser  
20 25 30

Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys  
35 40 45

<210> 24

<211> 17

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:  
Phosphatidylinositol-specific phospholipase X

<400> 24

Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser  
1 5 10 15

Cys

<210> 25

<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glypicans  
protein

<400> 25

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser  
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr

20 25 30  
 Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu  
 35 40 45

<210> 26  
 <211> 10  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Membrane attack  
 complex components/perforin

<400> 26  
 Ile Lys Asn Phe His Gln Tyr Ser Val Glu  
 1 5 10

<210> 27  
 <211> 44  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Urease nickel  
 ligands protein

<400> 27  
 Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu  
 1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro  
 20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys  
 35 40

<210> 28  
 <211> 13  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Phosphoglycerate  
 mutase family phosphohistidi

<400> 28  
 Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu  
 1 5 10

<210> 29  
 <211> 10  
 <212> PRT  
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ribosomal protein  
L23 protein

<400> 29

Glu Leu Arg Asp Leu Val Thr Gln Gln Leu  
1 5 10

<210> 30

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:  
2'-5'-oligoadenylate synthetases protein

<400> 30

Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu  
1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val  
20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His  
35 40

<210> 31

<211> 24

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Formate and  
nitrite transporters protein

<400> 31

Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly  
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu  
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<210> 32

<211> 34

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glycoprotein  
hormones beta chain protein

<400> 32

Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp

1                      5                      10                      15  
 Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser  
                     20                      25                      30

Val Glu

<210> 33  
 <211> 21  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Vinculin family  
           talin-binding region protein

<400> 33  
 Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln  
       1                      5                      10                      15

Leu Pro His Leu Met  
                     20

<210> 34  
 <211> 40  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Beta-lactamases  
           clas B protein

<400> 34  
 Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly  
       1                      5                      10                      15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln  
                     20                      25                      30

Leu Pro His Leu Met Pro Ser Asn  
                     35                      40

<210> 35  
 <211> 21  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Heat shock hsp20  
           protein family profile

<400> 35  
 Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser  
       1                      5                      10                      15

Val Lys Leu Glu Arg  
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<210> 36  
<211> 35  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:  
Hydroxymethylglutaryl-coenzyme A lyase protein

<400> 36  
Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser  
1 5 10 15  
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr  
20 25 30

Ser Val Glu  
35

<210> 37  
<211> 294  
<212> DNA  
<213> Mus sp.

<400> 37  
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caggttggca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180  
ggtgaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccaccct ccacggagta 240  
ctggtgaaag ttcttgatga ggggtctcaat ggccctctcc acatcactga attc 294

<210> 38  
<211> 43  
<212> PRT  
<213> Homo sapiens

<400> 38  
Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser  
1 5 10 15  
Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu  
20 25 30

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser  
35 40

<210> 39  
<211> 104  
<212> PRT  
<213> Homo sapiens translation of GenBank Accession AAY007220

<400> 39

Met	Gly	Gln	Cys	Arg	Ser	Ala	Asn	Ala	Glu	Asp	Ala	Gln	Glu	Phe	Ser
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			20					25					30		
Ser	Val	Glu	Gly	Gly	Lys	Glu	Thr	Leu	Thr	Pro	Ser	Glu	Leu	Arg	Asp
		35					40					45			
Leu	Val	Thr	Gln	Gln	Leu	Pro	His	Leu	Met	Pro	Ser	Asn	Cys	Gly	Leu
	50					55					60				
Glu	Glu	Lys	Ile	Ala	Asn	Leu	Gly	Ser	Cys	Asn	Asp	Ser	Lys	Leu	Glu
65					70					75					80
Phe	Arg	Ser	Phe	Trp	Glu	Leu	Ile	Gly	Glu	Ala	Ala	Lys	Ser	Val	Lys
			85						90					95	
Leu	Glu	Arg	Pro	Val	Arg	Gly	His								
			100												

<210> 40

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<400> 40

Met	Gly	Gln	Cys	Arg	Ser	Ala	Asn	Ala	Glu	Asp	Ala	Gln	Glu	Phe	Ser
1				5					10					15	
Asp	Val	Glu	Arg	Ala	Ile	Glu	Thr	Leu	Ile	Lys	Asn	Phe	His	Tyr	Ser
			20					25					30		
Val	Gly	Lys	Glu	Thr	Leu	Thr	Pro	Glu	Leu	Arg	Asp	Leu	Val	Thr	Gln
		35					40					45			
Gln	Leu	Pro	His	Leu	Met	Pro	Ser	Asn	Cys	Gly	Leu	Glu	Glu	Lys	Ile
	50					55					60				
Ala	Asn	Leu	Gly	Cys	Asn	Asp	Ser	Lys	Leu	Glu	Phe	Ser	Phe	Trp	Glu
65					70					75					80
Leu	Ile	Gly	Glu	Ala	Ala	Lys	Ser	Val	Lys	Glu	Arg	Pro	Val		
			85						90						

<210> 41  
<211> 41  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41  
Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly  
1 5 10 15  
Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu  
20 25 30  
Ile Asn Asn Glu Leu Ser His Phe Leu  
35 40

<210> 42  
<211> 41  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Protein MRP-126

<400> 42  
Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg  
1 5 10 15  
Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu  
20 25 30  
Ile Glu Lys Gln Leu Ala Asn Tyr Leu  
35 40

<210> 43  
<211> 41  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: ICTACALCIN

<400> 43  
Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Lys Tyr Ser Gly  
1 5 10 15  
Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu  
20 25 30  
Ile Thr Lys Glu Leu Gly Gly Ala Phe  
35 40

<210> 44  
<211> 41  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: CALGRANULIN B

<400> 44  
Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val  
1 5 10 15  
Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu  
20 25 30  
Val Gln Lys Glu Leu Pro Asn Phe Leu  
35 40

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<223> Description of Artificial Sequence: Consensus  
sequence

<400> 45  
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<210> 46  
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<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: CALGRANULIN B

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1 5 10 15  
Lys Glu Gly His Pro Asp Thr Leu Ser Lys Lys Glu Phe Arg Gln Met  
20 25 30  
Val Glu Ala Gln Leu Ala Thr Phe Met  
35 40

<210> 47  
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<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

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1 5 10

<210> 48

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<212> DNA

<213> Artificial Sequence

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<223> Description of Unknown Organism: reverse strand sequence of SEQ ID  
NO:4 (GenBank AA315020)

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<223> n is a, c, g, or t

<220>

<221> misc\_feature

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<223> n is a, c, g, or t

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